

IN THE CLAIMS

Please amend the claims as follows:

Claims 1-23 (Cancelled)

Claim 24 (Currently Amended): A method for predicting if a human cell has a decreased capacity to excrete compound B a drug transport capability of a mammalian cell, comprising:

collecting a biological sample from a human cell,

determining testing the biological sample from whether a mammalian said human cell for the presence of the genomic polynucleotide polymorphism of the ABCG2 gene in which C421A polymorphism occurs at nucleotide position 421 of SEQ ID NO: 1,

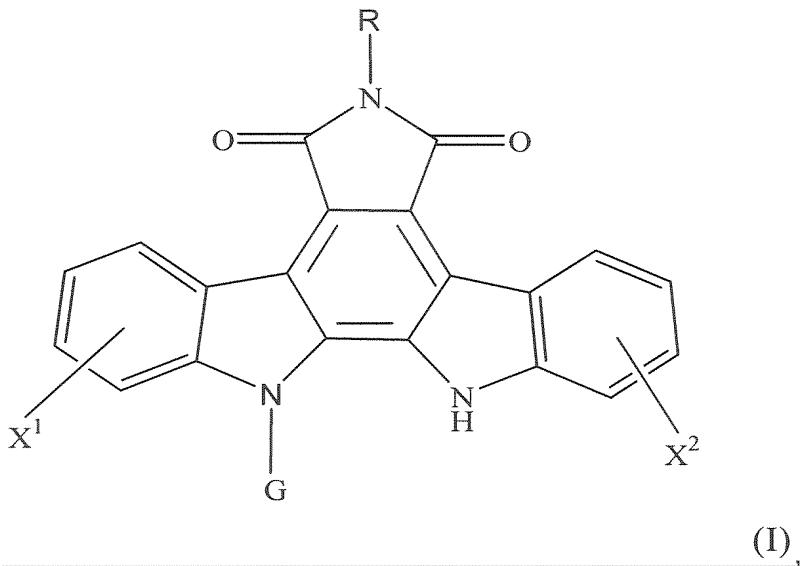
has a polymorphism at position 421 of the ABCG2 gene of SEQ ID NO: 1, or

determining whether an ABCG2 polypeptide produced by said mammalian cell has an amino acid substitution at position 141 of SEQ ID NO: 2;

wherein the presence of [[a]] said genomic polynucleotide polymorphism at position 421 an amino acid substitution at position 141 is indicative of a decreased capacity by said cell to excrete compound B

altered drug transport capability of said mammalian cell;

wherein compound B is a compound of formula (I):



wherein X¹ is 2-hydroxyl group,

X² is 10-hydroxyl group,

R is (1-hydroxymethyl-2-hydroxyl) ethylamino group,

G is beta-D-glucopyranosyl group.

Claims 25-28 (Cancelled)

Claim 29 (Currently Amended): The method of Claim 24, wherein the ~~mammalian~~
human cell is derived from a patient suffering from cancer.

Claim 30 (Currently Amended): The method of Claim 24, ~~further~~ comprising
collecting a ~~mammalian~~ cell sample from body fluid, skin, ~~hair~~ root of hair, mucous
membrane, internal organs, placenta, or cord blood of a subject prior to said ~~determining~~
testing step.

Claim 31 (Currently Amended): The method of Claim 24, which comprises detecting
[[a]] said genomic polynucleotide polymorphism by a direct sequencing method.

Claim 32 (Currently Amended): The method of Claim 24, which comprises detecting [[a]] said genomic polynucleotide polymorphism by a Taqman method.

Claim 33 (Currently Amended): The method of Claim 24, which comprises detecting [[a]] said genomic polynucleotide polymorphism by an invader method.

Claim 34 (Currently Amended): The method of Claim 24, which comprises detecting [[a]] said genomic polynucleotide polymorphism by a mass spectrometric method, an RCA method or a DNA chip method.

Claim 35-38 (Cancelled)

Claim 39 (Currently Amended): The method of Claim 24, further comprising determining testing whether a mammalian said human cell has at least one other genomic polynucleotide polymorphism in the ABCG2 gene of SEQ ID NO: 1, or determining whether an ABCG2 polypeptide produced by said mammalian cell has at least one other amino acid substitution of SEQ ID NO: 2.

Claim 40 (Currently Amended): The method of Claim 39, wherein said at least one other genomic polynucleotide polymorphism [[is]] occurs at nucleotide position 34 of SEQ ID NO: 1.

Claim 41 (Currently Amended): The method of Claim 39, wherein said at least one other genomic polynucleotide polymorphism [[is]] occurs at nucleotide position 376 of SEQ ID NO: 1.

Claim 42 (Currently Amended): The method of Claim 39, wherein said at least one other genomic polynucleotide polymorphism amino acid substitution [[is]] causes amino acid substitution at position 12 of SEQ ID NO: 2.

Claim 43 (Currently Amended): The method of Claim 39, wherein said at least one other amino acid substitution genomic polynucleotide polymorphism [[is]] causes amino acid termination at position 126 of SEQ ID NO: 2.

Claims 44-46 (Not Entered, Cancelled)

Claim 47 (New): The method of Claim 24, wherein said polymorphism is detected by a method using a fluorescent energy transfer phenomenon where hybridization of an allele-specific oligonucleotide to a template is performed simultaneously with PCR, comprising:

hybridizing an allele-specific probe which is labeled with a fluorescent dye and a quencher to a target site, simultaneously amplifying the region including the site whereupon the hybridization probe is cleaved by 5'-nuclease activity of Taq polymerase as the elongation reaction from the primer proceeds with PCR and detecting exponentially potentiated fluorescence of fluorescent dye which is separated from the quencher.

Claim 48 (New): The method of Claim 24, wherein said polymorphism is detected by a method comprising:

hybridizing a first probe which is substantially complementary to a first site of the target nucleotide sequence, hybridizing a second probe to a second site of the target nucleotide sequence where the second probe is complementary to its 3'-terminal side and a

sequence called a flap which is non-complementary to the template to form a single strand in its 5-terminal side, invading hybridization of the second probe with the target nucleotide sequence at an SNP site by the 3-terminal of the first probe, liberating the flap from the second probe by cleavase, binding of the flap to a FRET probe which includes a sequence complementary to the flap and self-complementary sequence being labeled with both a fluorescent dye and a quencher, cleaving the part of the fluorescent dye in the FRET probe by cleavase, quantifying fluorescence of the cleaved fluorescent dye.